MycoKeys 130: 265–286 (2026)
DOI: 10.3897/mycokeys.130.169753

Research Article

Morphological and phylogenetic analyses revealed *Cystidichaete alba* gen. et sp. nov. (Phanerochaetaceae, Polyporales) from Southwest China

Xunchi Zhang[1,2], Daxiang Chen[3], Changlin Zhao[1,2,4,5]

1 *Key Laboratory of Forest Disaster Warning and Control in Universities of Yunnan Province, Southwest Forestry University, Kunming 650224, China*
2 *College of Forestry, Southwest Forestry University, Kunming 650224, China*
3 *Yunnan Tongbiguan Provincial Nature Reserve, Mangshi 679319, China*
4 *Modern Industry School of Edible-fungi, Southwest Forestry University, Kunming 650224, China*
5 *Department Microbial Drugs (MWIS), Helmholtz-Centre for Infection Research, 38124 Braunschweig, Germany*

Corresponding author: Changlin Zhao (fungi@swfu.edu.cn; fungichanglinz@163.com)

Abstract

Wood-inhabiting fungi are a remarkably diverse group that play a fundamental role in ecosystem processes, particularly in wood degradation and the recycling of organic matter. As pivotal contributors to the intricate balance of forest ecosystems, these fungi are renowned as "key players" for their enzymatic prowess and products, which effectively breaks down woody components such as lignin, cellulose, and hemicelluloses. In the present study, a new wood-inhabiting fungal genus *Cystidichaete*, with its type species *C. alba*, collected from southwest China, is proposed based on a combination of morphological features and molecular evidence. The new genus *Cystidichaete* is characterized by the resupinate basidiomata with a smooth hymenophore, a monomitic hyphal system with clamped generative hyphae, abundant lamprocystidia, clavate basidia, and ellipsoid basidiospores. Sequences of the internal transcribed spacers (ITS), nuclear large subunit ribosomal RNA (nLSU), RNA polymerase second largest subunit (*rpb2*) and translation elongation factor 1-α (*tef1-α*) of the nuclear ribosomal DNA (rDNA) markers of the studied samples were generated. Phylogenetic analyses were performed using maximum likelihood, maximum parsimony, and Bayesian inference. Multi-locus phylogenetic analysis of ITS+nLSU+*rpb2*+*tef1-α* showed that *Cystidichaete* forms a monophyletic clade within the family Phanerochaetaceae (Polyporales), in which the new genus was grouped closely to *Stereophlebia* and *Gelatinofungus*.

Key words: Fungal classification, molecular systematics, new taxa, wood-inhabiting fungi

OPEN ACCESS

Academic editor: Yupeng Ge
Received: 25 August 2025
Accepted: 17 March 2026
Published: 27 March 2026

Citation: Zhang X, Chen D, Zhao C (2026) Morphological and phylogenetic analyses revealed *Cystidichaete alba* gen. et sp. nov. (Phanerochaetaceae, Polyporales) from Southwest China. MycoKeys 130: 265-286. https://doi.org/10.3897/mycokeys.130.169753

Copyright: © Xunchi Zhang et al.
This is an open access article distributed under terms of the Creative Commons Attribution License (Attribution 4.0 International – CC BY 4.0).

Introduction

Fungi are among Earth's most diverse groups of organisms, playing indispensable roles in ecosystem processes and functioning (Hyde 2022). Wood-inhabiting fungi, primarily basidiomycetes, hold significant industrial, edible, medicinal, nutritional and other economic values (Dai 2010; Wu et al. 2019; Dai et al. 2021; Niego et al. 2023; Yuan et al. 2023; Dong et al. 2024). These fungi colonize diverse woody substrates, including living trees, standing deadwood, fallen logs,

coarse branches, and stumps (M'Barek et al. 2020; Runnel et al. 2021; Dong et al. 2024). Wood-inhabiting fungi enzymatically degrade lignin, cellulose, and hemicelluloses through ligninolytic and cellulolytic enzymes, underscoring their critical role in organic matter recycling and nutrient cycling. These fungi are functionally categorized as white-rot or brown-rot taxa based on decay patterns (Bucher et al. 2004; Si et al. 2011; An et al. 2015; Liu et al. 2023).

Fungal classification within the kingdom Fungi is continually revised, driven by the integration of DNA sequence data into modern phylogenetic studies (Cui et al. 2019; Wijayawardene et al. 2020, 2022; Hyde et al. 2024; Dong et al. 2024). Given the early embrace of molecular systematics by mycologists, both the discovery and classification of fungi, among the more basal branches of the tree, are now emerging from genomic analyses and environmental DNA surveys (James et al. 2020).

Species of the family Phanerochaetaceae Jülich belong to wood inhabiting fungi, and they have industrial, medicinal, edible, and economic values while some others contain toxic metabolites (Chen et al. 2021; Dong et al. 2024; Xu et al. 2025). They produce ligninolytic and cellulolytic enzymes that break down lignin, cellulose, and hemicelluloses, underscoring their significance in the recycling of organic matter and nutrient cycling, typically categorized as the white-rot and brown-rot fungi (Cui et al. 2019; Chen et al. 2021).

The family Phanerochaetaceae belonging to the order Polyporales (Basidiomycota), was typified by *Phanerochaete* P. Karst. Twenty-eight genera were placed in this family Phanerochaetaceae as *Alboefibula* C.C. Chen & Sheng H. Wu, *Bjerkandera* P. Karst., *Callosus* C.L. Zhao, *Cremeoderma* Sheng H. Wu & C.C. Chen, *Crepatura* C.L. Zhao, *Donkia* Pilát, *Donkiella* J.H. Dong & C.L. Zhao, *Efibulella* Zmitr., *Gelatinofungus* Sheng H. Wu, et al., *Geliporus* Yuan Yuan, et al., *Hapalopilus* P. Karst., *Hyphodermella* J. Erikss. & Ryvarden, *Odontoefibula* C.C. Chen & Sheng H. Wu, *Oxychaete* Miettinen, *Paradonkia* Y. Xu & C.L. Zhao, *Neodonkiella* Y. Xu & C.L. Zhao, *Phaeophlebiopsis* Floudas & Hibbett, *Phanerina* Miettinen, *Phanerochaete* P. Karst., *Phlebiopsis* Jülich, *Pirex* Hjortstam & Ryvarden, *Porostereum* Pilát, *Quasiphlebia* C.C. Chen & Sheng H. Wu, *Rhizochaete* Gresl., Nakasone & Rajchenb., *Riopa* D.A. Reid, *Roseograndinia* Hjortstam & Ryvarden, *Stereophlebia* Zmitr. and *Terana* Adans according to recent studies (Dong et al. 2024; He et al. 2024; Larsson et al. 2025; Xu et al. 2025). Pioneering studies have been conducted on the phylogenetic analyses of Phanerochaetaceae, especially in *Phanerochaete* (Floudas and Hibbett 2015; Miettinen et al. 2016; Xu et al. 2020; Chen et al. 2021; Deng et al. 2024; Dong et al. 2024; Xu et al. 2025). The research using RPB1, RPB2, and the ITS and LSU ribosomal genes to investigate phanerochaetoid taxa and revealed that four clades of *Phanerochaete* sensu stricto, *Bjerkandera*, *Hyphodermella* and *Phlebiopsis* were divided, in which *Phanerochaete* s.s. and *Phlebiopsis* clades have been previously identified (Floudas and Hibbett 2015). Miettinen et al. (2016) carried on the phylogenetic relationships among genera within Phanerochaetaceae based on phylogenetic analyses of ITS, LSU and RPB1, which showed that the macromorphology of basidiomata and hymenophore construction did not reflect monophyletic groups in *Phanerochaete*. Further phylogeny of the five corticicoid genera of Phanerochaetaceae based on ITS1-5.8S-ITS2 and nrLSU sequence data showed that the *Donkia*, *Phlebiopsis*, *Rhizochaete*, and *Phanerochaete* clades formed a distinct lineage. Based on the ITS+nLSU rDNA gene regions, the research revealed that three species of *P. albocremea* Ying Xu & C.L.

Zhao, *P. fissurata* Ying Xu & C.L. Zhao, and *P. punctata* Ying Xu & C.L. Zhao were located in the family *Phanerochaetaceae*, in which the species *P. fissurata* was retrieved as a sister to *P. cinerea* (Xu et al. 2025).

The corticioid species are the predominant morphological type in Phanerochaetaceae, but some have resupinated polypores and hydnaceous species (Chen et al. 2021; Zhao et al. 2024). The hyphal system of this family is usually monomitic, rarely dimitic, and the generative hyphae are usually simple septate, rarely nodose-septate, and cystidia are often present, and basidiospores are usually thin-walled, smooth, and colorless (Justo et al. 2017; Chen et al. 2021).

During investigations on wood-inhabiting fungi in the Yunnan-Guizhou Plateau, China, a large number of corticioid specimens were collected. To clarify the placement and relationships of these specimens, molecular phylogenetic along with taxonomic studies were carried out on the family Phanerochaetaceae based on the combined ITS+nLSU+*rpb2*+*tef1-α* data analysis. Accordingly, *Cystidichaete* gen. nov. (Phanerochaetaceae, Polyporales) and its novel species *C. alba* sp. nov. are formally described here, supported by morphological illustrations and multi-locus phylogeny.

Materials and methods

Sample collection and herbarium specimen preparation

The basidiomata were collected from fallen angiosperm branches in the Dehong Dai and Jingpo Autonomous Prefecture of Yunnan Province, Southwest China. The samples were photographed *in situ*, and fresh macroscopic details and other important information were recorded (Rathnayaka et al. 2025). Photographs were recorded by a Xiaomi 14 Ultra camera. Macroscopic observations were noted. Collected basidiomata were dried on an electric food dryer at 40 °C. Dried specimens were sealed in envelopes and zip-lock plastic bags and labeled with voucher numbers (Dong et al. 2025a). The voucher specimens were deposited in the herbarium of the Southwest Forestry University (SWFC), Kunming, Yunnan Province, P.R. China.

Morphological study

The macro-morphological descriptions were based on field notes and photos taken in the field and in the lab. The color terminology follows Petersen (1996) and was confirmed in general terms according to the CMYK color code (Deep White Printing Team 2022). The micro-morphological data were obtained from dried specimens observed under a light microscope at 10 × 100 magnification (Zhao et al. 2023). Sections were mounted in 5% KOH and 2% Phloxine B ($C_{20}H_2Br_4C_{l4}N$-a_2O_5) for microscopic observation. Cotton Blue and Melzer's reagent were also used to examine micromorphological structures. Congo red was used as a stain when necessary (Horak 2005). To show the variation in spore sizes, 5% of measurements were excluded from each end of the range and shown in parentheses. At least 30 basidiospores from each specimen were measured. The following abbreviations are used: **KOH** = 5% potassium hydroxide water solution, **CB–** = acyanophilous, **IKI–** = both inamyloid and indextrinoid, **L** = mean spore length (arithmetic average for all spores), **W** = mean spore width (arithmetic average for

all spores), **Q** = variation in the L/W ratios between the specimens studied, **Qm** represented the average Q of basidiospores measured ± standard deviation, and **n** = a/b (number of spores (a) measured from given number (b) of specimens).

Molecular phylogenetic studies

The CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd, Beijing, China) was used to obtain genomic DNA from the dried fungal specimens according to the manufacturer's instructions (Dong et al. 2024; Yang et al. 2025b). The extracted DNA was maintained at –20 °C for long-term storage. Four molecular markers were investigated, i.e., internal transcribed spacer (ITS), nuclear large subunit ribosomal RNA (nLSU), RNA polymerase II subunit 2 (*rpb2*) gene, and Translation elongation factor 1-α (*tef1-α*) gene and the primers and conditions are shown in Table 1. The PCR products were purified and sequenced at Kunming Tsingke Biological Technology Limited Company (Yunnan Province, China). All newly generated sequences were deposited in NCBI GenBank (https://www.ncbi.nlm.nih.gov/genbank/) (Table 2).

Sequences generated for this study were aligned, with additional sequences downloaded from GenBank. Sequences were aligned in MAFFT 7 (https://mafft.cbrc.jp/alignment/server/) adjusting the direction of nucleotide sequences according to the first sequence (accurate enough for most cases), and selecting the G-INS-i iterative refinement method (Katoh et al. 2019). The alignment was adjusted manually using AliView version 1.27 (Larsson 2014). The dataset was first aligned, and then the sequences of ITS+nLSU+*rpb*2+ *tef*1-α were combined in Mesquite v. 3.81. The combined ITS+nLSU+*rpb2*+ *tef1-α* dataset was used to infer the phylogenetic analysis of the new genus and related species within the Phanerochaetaceae. For this analysis, *Irpex lacteus* (Fr.) Fr. *and Irpex latemarginatus* (Durieu & Mont.) C.C. Chen & Sheng H. Wu served as the outgroup to root the tree (Fig. 1; Dong et al. 2024). The alignment datasets were deposited in TreeBASE (Submission ID 32269).

Table 1. Loci, primers, PCR amplification procedures, and references used in this study.

Name	Abbreviation	Name	Direction	Sequence (5'-3')	PCR amplification procedures	References
Internal transcribed spacer region of the rDNA	ITS	ITS5	Forward	GGAAGTAAAAGTCGTAACAAGG	94 °C 2 min; 35 cycles of 94 °C 60 s, 55 °C 60 s, 72 °C 2 min; 72 °C 10 min.	White et al. (1990)
		ITS4	Reverse	TCCTCCGCTTATTGATATGC		
Nuclear large subunit ribosomal	nLSU	LR0R	Forward	ACCCGCTGAACTTAAGC	94 °C 2 min; 35 cycles of 94 °C 30 s, 48 °C 1 min, 72 °C 1.5 min; 72 °C 10 min.	Vilgalys and Hester (1990)
		LR7	Reverse	TACTACCACCAAGATCT		
RNA polymerase second largest subunit	*rpb2*	RPB2-6F	Forward	TGGGGYATGGTNTGYCCYGC	94 °C 2 min; 9 cycles of 94 °C 45 s, 60 °C 45 s, 72 °C 1.5 min; 36 cycles of 94 °C 45 s, 53 °C 1 min, 72 °C 1.5 min; 72 °C 10 min.	Liu et al. (1999)
		RPB2-7cR	Reverse	CCCATRGCTTGYTTRCCCAT		
Translation elongation factor 1-α	*tef1*-α	EF1-983 F	Forward	GCYCCYGGHCAYCGTGAYTTYAT	94 °C 1 min; 35 cycles of 94 °C 30 s, 59 °C 1 min, 72 °C 1.5 min; 72 °C 10 min.	Rehner and Buckley (2005)
		EF1-2218R	Reverse	ATGACACCRACRGCRACRGTYTG		

Table 2. Names, voucher numbers, localities, references, and corresponding GenBank accession numbers of the taxa used in this study. New species are shown in bold; * refers to type material (holotype) and — refers to the missing data.

Species Name	Sample no.	GenBank Accession No.				Origin	References
		ITS	nLSU	*rpb2*	*tef1-α*		
Alboefibula bambusicola	Chen 2304*	MZ636926	MZ637091	OK135980	MZ913590	China	Chen et al. (2021)
Alboefibula gracilis	Wu 1809-106*	MZ636929	MZ637094	OK135982	MZ913591	China	Chen et al. (2021)
Bjerkandera adusta	HHB-12826-Sp	KP134983	KP135198	KP134913	KT305938	USA	Floudas and Hibbett (2015)
Bjerkandera centroamericana	L-13104-sp	KY948791	KY948855	—	—	Costa Rica	Justo et al. (2017)
Callosus wenshanensis	CLZhao 16017*	MW553934	MW553936	—	—	China	Chen et al. (2022)
Callosus wenshanensis	CLZhao 16034	MW553935	MW553937	—	—	China	Chen et al. (2022)
Cremeoderma unicum	Wu 1707-94	MZ636939	MZ637102	OK135987	MZ913705	China	Chen et al. (2021)
Cremeoderma unicum	Wu 1707-100	MZ636938	MZ637101	—	—	China	Chen et al. (2021)
Crepatura ellipsospora	CLZhao 1265*	MK343692	MK343696	—	—	China	Ma and Zhao (2019)
Crepatura ellipsospora	CLZhao 1260	MK343693	MK343697	—	—	China	Ma and Zhao (2019)
Cystidichaete alba	**CLZhao 39422**	**PX092380**	**PX092378**	**PX108328**	**PX108329**	China	**Present study**
Cystidichaete alba	**CLZhao 39667***	**PX092381**	**PX092379**	**—**	**—**	China	**Present study**
Donkia pulcherrima	GC 1707-11	LC378994	LC379152	LC387351	LC387371	China	Chen et al. (2018)
Donkia pulcherrima	Gothenburg-2022	KX752591	KX752591	—	—	Austria	Miettinen et al. (2016)
Donkiella yunnanensis	CLZhao 3931*	OR094482	OR461467	OR733285	OR541925	China	Dong et al. (2024)
Donkiella yunnanensis	CLZhao 18292	OR094483	OR461468	OR733286	OR541926	China	Dong et al. (2024)
Efibulella deflectens	FCUG 1568	AF141619	AF141619	—	—	Sweden	Parmasto and Hallenberg (2000)
Gelatinofungus brunneus	GC 1703-31*	LC387339	LC387344	LC387367	LC387385	China	Chen et al. (2018)
Gelatinofungus brunneus	Wu 1207-162	MZ636978	MZ637139	OK136005	MZ913615	China	Chen et al. (2021)
Gelatinofungus sp.	RLG-10795-Sp	KY948785	KY948857	OK136007	MZ913619	USA	Justo et al. (2017)
Geliporus exilisporus	Dai 2172	KU598211	KU598216	—	—	China	Yuan et al. (2017)
Geliporus exilisporus	GC 1702-15	LC378995	LC379153	LC387352	LC387372	China	Chen et al. (2018)
Hapalopilus percoctus	H 7008581*	KX752597	KX752597	—	—	Botswana	Miettinen et al. (2016)
Hapalopilus rutilans	FP-102473-Sp	MZ636981	MZ637142	OK136004	MZ913723	USA	Chen et al. (2021)
Hyphodermella corrugata	MA-Fungi 24238	FN600378	JN939586	—	—	Portugal	Telleria et al. (2010)
Hyphodermella rosae	GC 1604-113	MZ636986	MZ637147	—	—	China	Chen et al. (2021)
Hyphodermella rosae	GC 1608-2	MZ636987	MZ637148	OK135983	MZ913592	Japan	Chen et al. (2021)
Irpex lacteus	FD-9	KP135026	KP135224	—	—	USA	Floudas and Hibbett (2015)
Irpex latemarginatus	FP-55521-T	KP135024	KP135202	KP134915	—	USA	Floudas and Hibbett (2015)
Odontoefibula orientalis	Wu 0910-57*	LC363490	LC363495	LC387362	LC387381	China	Chen et al. (2018)
Odontoefibula orientalis	GC 1703-76	LC379004	LC379156	LC387360	LC387379	China	Chen et al. (2018)
Oxychaete cervinogilva	GC 1501-16	MZ422783	MZ637173	—	MZ913613	China	Chen et al. (2021)
Oxychaete cervinogilva	Dmitry Schigel 5216	KX752596	KX752596	—	—	Australia	Chen et al. (2021)
Paradonkia farinacea	CLZhao 27184*	PQ527890	PQ527887	—	—	China	Xu et al. (2025)
Paradonkia farinacea	CLZhao 27221	PQ527891	PQ527888	—	—	China	Xu et al. (2025)
Neodonkiella yinjiangensis	CLZhao 30585*	PQ527892	PQ527889	—	—	China	Xu et al. (2025)
Phaeophlebiopsis caribbeana	HHB-6990	KP135415	KP135243	KP134931	MZ913643	USA	Floudas and Hibbett (2015)
Phaeophlebiopsis peniophoroides	FP-150577	KP135417	KP135273	—	—	USA	Floudas and Hibbett (2015)

Species Name	Sample no.	GenBank Accession No.				Origin	References
		ITS	nLSU	*rpb2*	*tef1-α*		
Phanerina mellea	Wu 1010-34	MZ422784	MZ637176	—	—	China	Chen et al. (2021)
Phanerina mellea	WEI 17-224	LC387333	LC387340	LC387363	LC387382	China	Chen et al. (2018)
Phanerochaete australis	GC 1505-15	MZ422792	MZ637184	OK136010	MZ913595	China	Chen et al. (2021)
Phanerochaete velutina	GC 1604-56	MZ422844	MZ637224	OK136015	MZ913642	China	Chen et al. (2021)
Phlebiopsis gigantea	FCUG 1417	MZ637051	AF141634	OK135996	MZ913623	Norway	Liu et al. (2023)
Phlebiopsis crassa	GC 1602-45	MZ637049	MZ637251	OK135999	MZ913626	China	Chen et al. (2021)
Pirex concentricus	Kropp160Bup6-R	KP134985	—	—	—	USA	Floudas and Hibbett (2015)
Pirex concentricus	OSC-41587	KP134984	KP135275	KP134940	—	USA	Floudas and Hibbett (2015)
Porostereum fulvum	LY:18491	MG649452	MG649454	—	—	France	Chen et al. (2021)
Porostereum spadiceum	Wu 9508-139	MZ637062	MZ637263	OK136067	MZ913697	China	Chen et al. (2021)
Quasiphlebia densa	WEI 17-057	MZ637066	MZ637265	OK135986	MZ913630	China	Chen et al. (2021)
Quasiphlebia densa	Wu 9304-33	MZ637067	MZ637266	—	—	China	Chen et al. (2021)
Rhizochaete filamentosa	HHB-3169	KP135410	KP135278	KP134935	—	USA	Floudas and Hibbett (2015)
Rhizochaete radicata	FD-123	KP135407	KP135279	KP134937	—	USA	Floudas and Hibbett (2015)
Riopa metamorphosa	Spirin 2395	KX752601	KX752601	—	—	Russia	Miettinen et al. (2016)
Riopa pudens	Cui 3238	JX623931	JX644060	—	—	China	Jia et al. (2014)
Roseograndinia jilinensis	Wu 1307-137*	MZ637077	MZ637275	OK135985	MZ913632	China	Chen et al. (2021)
Roseograndinia minispora	WEI 18-508*	MZ637078	MZ637276	—	—	China	Chen et al. (2021)
Stereophlebia pendula	GB:KHL 15159	PQ013066	PQ013066	—	—	Spain	Larsson et al. (2025)
Stereophlebia pendula	GB:EL 29-11	PQ013067	PQ013067	—	—	Spain	Larsson et al. (2025)
Terana caerulea	FP-104073	KP134980	KP135276	KP134960	—	USA	Floudas and Hibbett (2015)
Terana caerulea	GC 1507-2	MZ637090	MZ637287	OK136037	MZ913654	China	Chen et al. (2021)

Maximum Parsimony (MP), Maximum Likelihood (ML), and Bayesian Inference (BI) analyses were applied to the combined three datasets following previous studies (Zhao and Wu 2017; Yang et al. 2025a). Maximum Parsimony (MP) analysis was performed in PAUP* v. 4.0b10 (Swofford 2002). All characters were equally weighted, and gaps were treated as missing data. Trees were inferred using the heuristic search option with TBR branch swapping and 1000 random sequence additions. Max trees were set to 5000, branches of zero length were collapsed, and all parsimonious trees were saved. Clade robustness was assessed using bootstrap (BT) analysis with 1000 replicates (Felsenstein 1985). Descriptive tree statistics, tree length (TL), consistency index (CI), retention index (RI), rescaled consistency index (RC), and homoplasy index (HI) were calculated for each maximum parsimonious tree generated. Maximum likelihood (ML) analysis was performed with RAxML-HPC BlackBox in CIPRES Science Gateway (https://www.phylo.org/portal2/login!input.action, Miller et al. 2012) using a GTRCAT model of evolution with 1,000 bootstrap replicates. ModelFinder v2.2.0 (Kalyaanamoorthy et al. 2017) was used to select the best-fit model using Bayesian Information Criterion (BIC). Bayesian Inference (BI) phylogenies by PhyloSuite v1.2.3 (Zhang et al. 2020; Xiang et al. 2023) were inferred using MrBayes v3.2.7a (Ronquist et al. 2012). Branches were considered significantly supported if they received a Maximum Likelihood bootstrap value (BS) of ≥ 70%, a Maximum Parsimony bootstrap value (BT) of ≥ 50%, or Bayesian Posterior Probabilities (BPP) of ≥ 0.95.

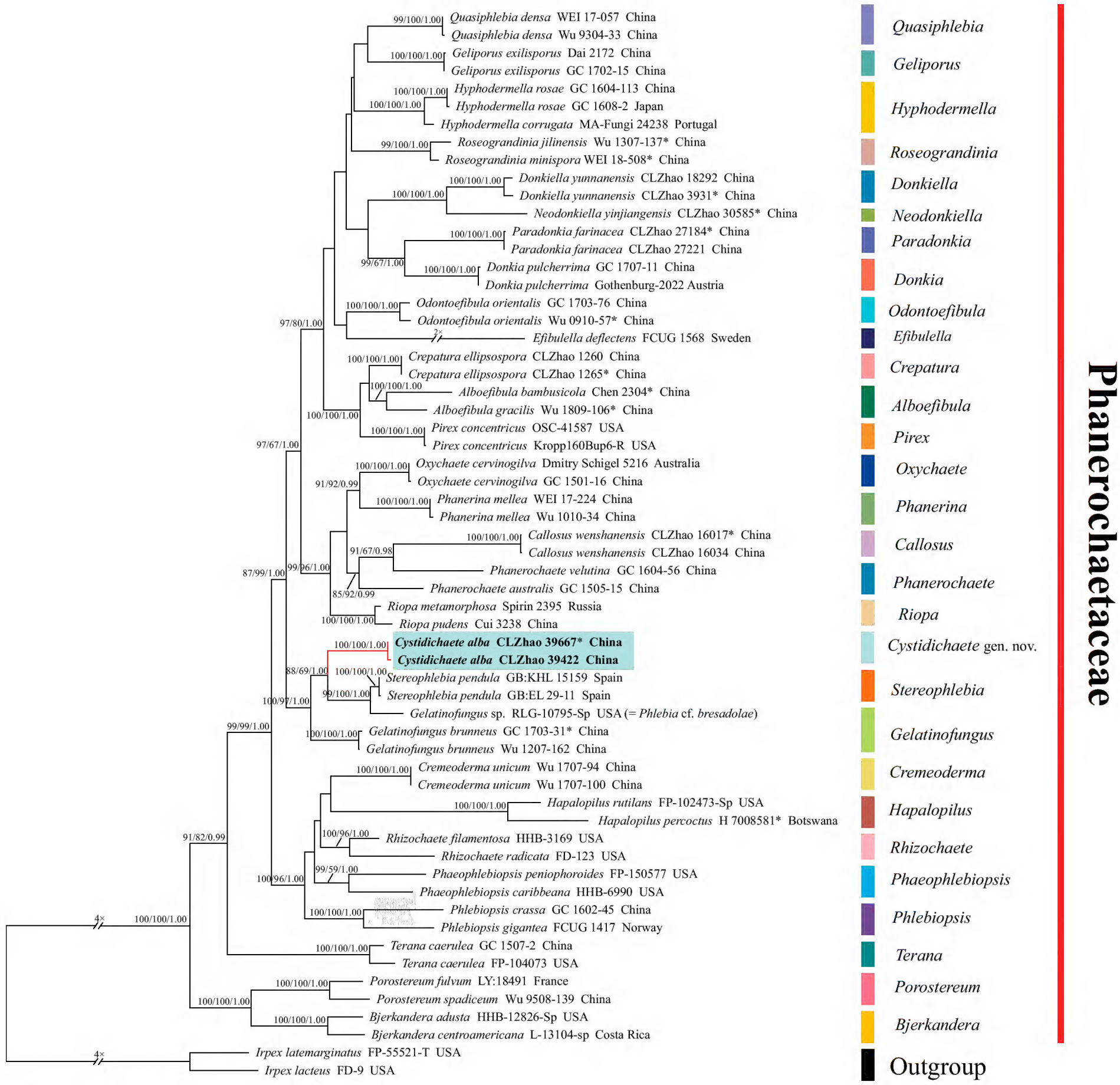

Figure 1. Maximum Likelihood analysis illustrating the phylogeny of *Cystidichaete* and related genera in the family Phanerochaetaceae based on ITS+nLSU+*rpb2*+*tef1-α* sequences. Branches are labelled with maximum likelihood bootstrap value ≥ 70%, parsimony bootstrap value ≥ 50%, and Bayesian posterior probabilities ≥ 0.95. Colored bars represent different genera. New species are shown in bold, * refers to type material (holotype).

Results

Phylogenetic analyses

The combined ITS+nLSU+*rpb2*+ *tef1-α* dataset (Fig. 1) included sequences from 60 fungal specimens representing 43 species. The dataset had an aligned length of 3987 characters, of which 2504 were constant, 316 were variable and parsimony-uninformative, and 1167 were parsimony-informative. Maximum Parsimony (MP) analysis yielded one equally parsimonious tree (TL = 6874, CI = 0.3667, HI = 0.6333, RI = 0.4944, and RC = 0.1813).

Table 3. Summary of NCBI BLAST results for *Cystidichaete alba* based on ITS, nLSU, *rpb2*, and *tef1-α* sequences (accessed on 25 August 2025).

Gene Locus	Top Ten Similar Taxa with Significant Alignments	Maximum Record Descriptions					References
		Max Score	Total Score	Query Cover	E value	Identity	
ITS	*Stereophlebia pendula* (Fr.) K.H. Larss.	1005	1005	97%	0	95.71%	Larsson et al. (2025)
nLSU	*Stereophlebia pendula* (Fr.) K.H. Larss.	2438	2438	98%	0	99.04%	Larsson et al. (2025)
	Gelatinofungus betulina Shun Liu & Biao Zhu						Liu et al. (2025)
	Gelatinofungus sp. strain RLG-10795-Sp						Justo et al. (2017)
	Phlebiopsis daweishanensis J.H. Dong & C.L. Zhao						Dong et al. (2024)
	Phlebiopsis xuefengensis J. Zou						Li et al. (2021)
	Riopa pudens Miettinen						Dai YC lab submission
	Phlebiopsis pilatii (Parmasto) Spirin & Miettinen						Miettinen et al. (2016)
	Ceriporia mellea (Berk. & Broome) Ryvarden						Jia et al. (2014)
rpb2	*Gelatinofungus* sp. strain RLG-10795-Sp	651	651	100%	0	82.64%	Chen et al. (2021)
	Gelatinofungus brunneus Sheng H. Wu, C.C. Chen & C.L. Wei						Chen et al. (2021)
	Phanerochaete ericina (Bourdot) J. Erikss. & Ryvarden						Floudas and Hibbett (2015)
	Phanerochaete thailandica Kout & Sádlíková						Chen et al. (2021)
	Phlebiopsis alpina C.C. Chen, Sheng H. Wu & S.H. He						Chen et al. (2021)
	Ceriporia camaresiana (Bourdot & Galzin) Bondartsev & Singer						Větrovský et al. (2016)
tef1-α	*Gelatinofungus brunneus* Sheng H. Wu, C.C. Chen & C.L. Wei	1476	1476	100%	0	92.82%	Chen et al. (2021)
	Gelatinofungus sp. strain RLG-10795-Sp						Justo et al. (2017)
	Terana caerulea (Lam.) Kuntze						Chen et al. (2021)
	Peniophora nuda (Fr.) Bres., Plicaturopsis crispa (Pers.) D.A. Reid						Brandon Matheny et al. (2007)
	Panaeolina foenisecii (Pers.) Maire						Direct Submission

The best RAxML tree with a final likelihood value of -33260.831640 is presented. The evolutionary model GTR+GAMMA is applied to all the genes. The matrix contained 1762 distinct alignment patterns, with 38.82% of characters undetermined (gaps). Estimated base frequencies were as follows: A = 0.243058, C = 0.238649, G = 0.272340, T = 0.245954; substitution rates AC = 0.884598, AG = 2.826789, AT = 1.650582, CG = 0.888040, CT = 5.769647, GT = 1.000000; gamma distribution shape parameter α = 0.217174.

The best-fit model for the dataset according to BIC: GTR+I+G4. Bayesian analysis was performed under the GTR+I+G4 model (2 parallel runs, 1000000 generations), in which the initial 25% of sampled data were discarded as burn-in. Both Bayesian Inference (BI) and Maximum Parsimony (MP) analyses resulted in a similar topology to the Maximum Likelihood (ML) analysis, with an average standard deviation of split frequencies = 0.007990 (BI), and the effective sample size (ESS) for Bayesian analysis across the two runs is the double of the average ESS (avg. ESS) = 579.5.

Based on separate analyses of ITS, nLSU, *rpb2*, and *tef1-α* sequences, NCBI BLAST searches performed on 25 August 2025 returned the top ten similar taxa with significant alignments (Table 3).

The topology based on ITS+nLSU+rpb2+ tef1-α sequences (Fig. 1) showed that the new taxon was clustered into Phanerochaetaceae, with which it formed a distinct lineage, and sister to *Stereophlebia* and *Gelatinofungus* with 100% BS, 97% BP, 1.00 BPP support. Accordingly, we introduce *Cystidichaete* gen. nov., with *Cystidichaete alba* sp. nov. designated as the type species.

Taxonomy

Phanerochaetaceae Jülich

Type genus. *Phanerochaete* P. Karst.

Description. Mostly corticioid species, along with a few resupinate or pileate polypores, and pileate hydnaceous species; hyphal system usually monomitic, rarely dimitic; hyphae usually simple septate, rarely nodose-septate; basidiospores thin-walled, smooth, colorless; cystidia often present. Producing a white rot. (Chen et al. 2021).

Accepted genera. *Alboefibula*, *Bjerkandera*, *Callosus*, *Cremeoderma*, *Crepatura*, *Cystidichaete*, *Donkia*, *Donkiella*, *Efibulella*, *Gelatinofungus*, *Geliporus*, *Hapalopilus*, *Hyphodermella*, *Odontoefibula*, *Oxychaete*, *Paradonkia*, *Neodonkiella*, *Phanerina*, *Phanerochaete*, *Phaeophlebiopsis*, *Phlebiopsis*, *Pirex*, *Porostereum*, *Quasiphlebia*, *Rhizochaete*, *Riopa*, *Roseograndinia*, *Stereophlebia* and *Terana*.

Notes. Phanerochaetaceae was established by Jülich (1982) with the genus *Phanerochaete* as the type genus. It belongs to the phlebioid clade within the order Polyporales and causes a white rot (Larsson 2007; Binder et al. 2013; Miettinen et al. 2016; Justo et al. 2017). In the current study, 29 genera are accepted in Phanerochaetaceae, *Cystidichaete* gen. nov., which is newly proposed in this study.

Cystidichaete X.C. Zhang & C.L. Zhao, gen. nov.

MycoBank No: 860430

Chinese name. 囊状体革菌属 (nang zhuang ti ge jun shu).

Etymology. *Cystidichaete* (Lat.): refers to the abundant cystidia in the hymenium.

Description. Basidiomata annual, resupinate, adnate, membranaceous, without odor or taste when fresh, becoming fragile upon drying. Hymenial surface smooth, white when fresh, white to cream when dry. Hyphal system monomitic; generative hyphae with clamp connections, colorless, thin- to slightly thick-walled. Subicular hyphae thin- to slightly thick-walled. Lamprocystidia abundant, arising from subhymenium, subulate, heavily encrusted with crystals, distinctly thick-walled, embedded in subhymenium or exerted. Basidia clavate, occasionally with oil drops, with four sterigmata and a basal clamp connection. Basidiospores ellipsoid, colorless, thin-walled, smooth, occasionally with oil drops, IKI–, CB–. Causing a white rot.

Type species. *Cystidichaete alba* X.C. Zhang & C.L. Zhao.

Notes. In our analyses, *Cystidichaete* is formed a distinct group typified by *C. alba*. The new genus placed within Phanerochaetaceae (Polyporales) and grouped with *Stereophlebia* and *Gelatinofungus* with 100% BS, 97% BP, 1.00 BPP support (Fig.1). However, morphologically, *Stereophlebia* differs from *Cystidichaete* by having chondrostereoid to phlebioid basidiomata, prostrate to reflexed with differentiated upper tomentum, a smooth or irregularly costate to tuberculate hymenophore, and lacking lamprocystidia (Zmitrovich 2018). *Gelatinofungus* differs from *Cystidichaete* by having ceraceous basidiomata, a dark purplish gray to cinnamon-brown hymenial surface that darkens in KOH, a smooth to tuberculate hymenophore, and lacking lamprocystidia (Chen et al. 2021).

Cystidichaete alba **X.C. Zhang & C.L. Zhao, sp. nov.**
MycoBank No: 860431
Figs 2, 3, 4

Chinese name. 白囊状体革菌 (bai nang zhuang ti ge jun).

Holotype. China • Yunnan Province, Dehong Dai and Jingpo Autonomous Prefecture, Mangshi, Tongbiguan Nature Reserve, GPS coordinates 24°22'N, 97°50'E, altitude 1405 m asl., on fallen angiosperm branch, leg. C.L. Zhao, 8 July 2024, CLZhao 39667 (SWFC 00039667).

Etymology. *alba* (Lat.): refers to the species having a white hymenial surface.

Basidiomata. Annual, resupinate, closely adnate, membranaceous, without odor or taste when fresh, becoming fragile upon drying, up to 8 cm long, 2 cm wide, and 160 μm thick. Hymenial surface smooth, white (C0 M0 Y5 K0) when fresh, white (C0 M0 Y5 K0) to cream (C0 M5 Y30 K0) upon drying. Sterile margin grayish-white (C0 M0 Y0 K5), narrow, up to 2 mm wide.

Hyphal structure. Monomitic, generative hyphae with clamp connections, colorless, thin- to slightly thick-walled, branched, interwoven, 2–3.5 μm in diameter; ubicular hyphae thin- to slightly thick-walled 3–3.5 μm in diameter. IKI–, CB–; tissues unchanged in KOH.

Hymenium. Lamprocystidia abundant, arising from subhymenium, subulate, heavily encrusted with crystals, distinctly thick-walled, embedded in subhymenium or exerted, 35–68 × 8–15 μm. Basidia clavate, occasionally with oil drops, with four sterigmata and a basal clamp connection, 13–20× 4–6 μm; basidioles dominant, occasionally with oil drops, similar to basidia in shape, but slightly smaller.

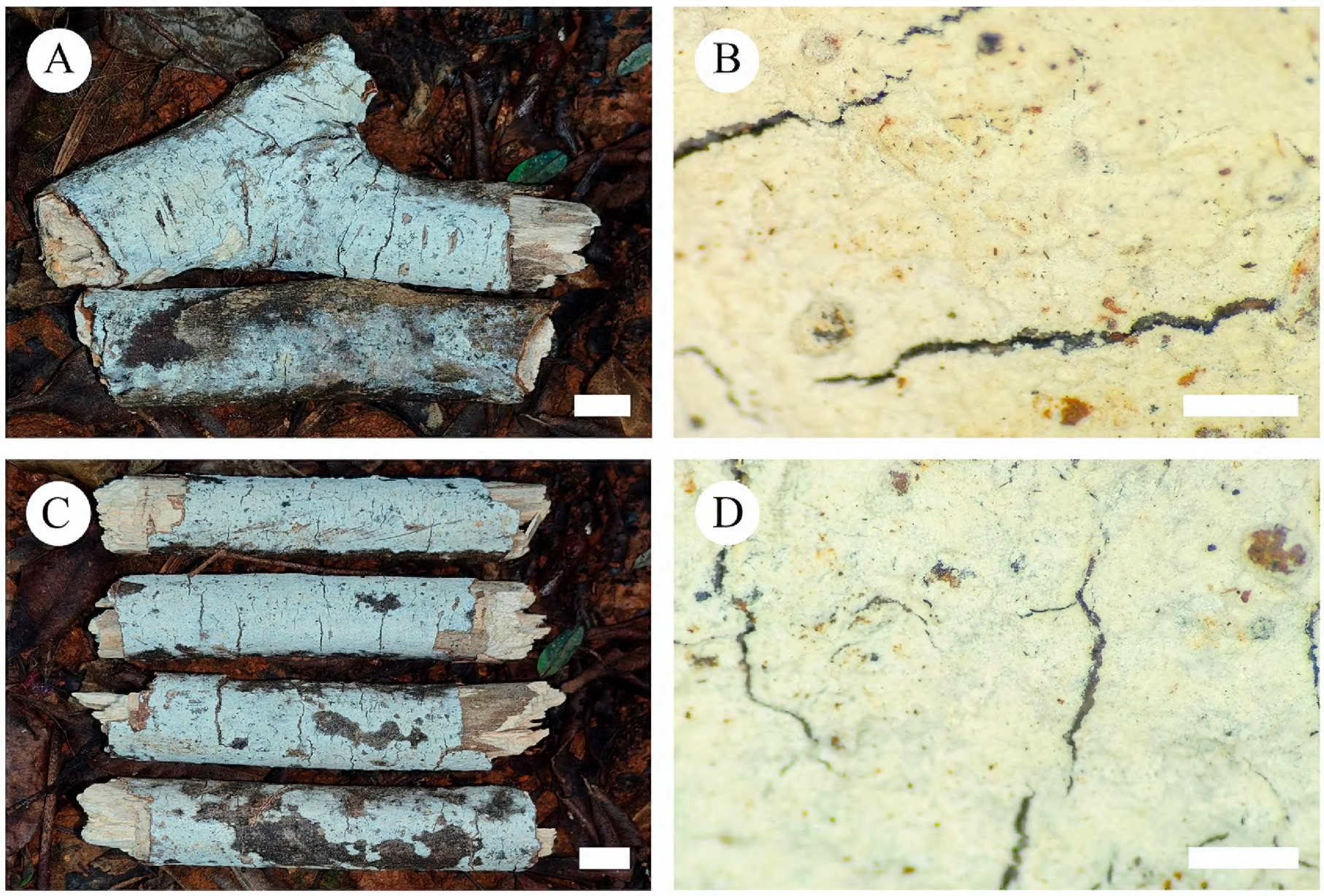

Figure 2. Basidiomata of *Cystidichaete alba*, in general and in detail. **A, B.** CLZhao 39422; **C, D.** CLZhao 39667 (holotype). Scale bars: 1 cm (**A, C**); 1 mm (**B, D**).

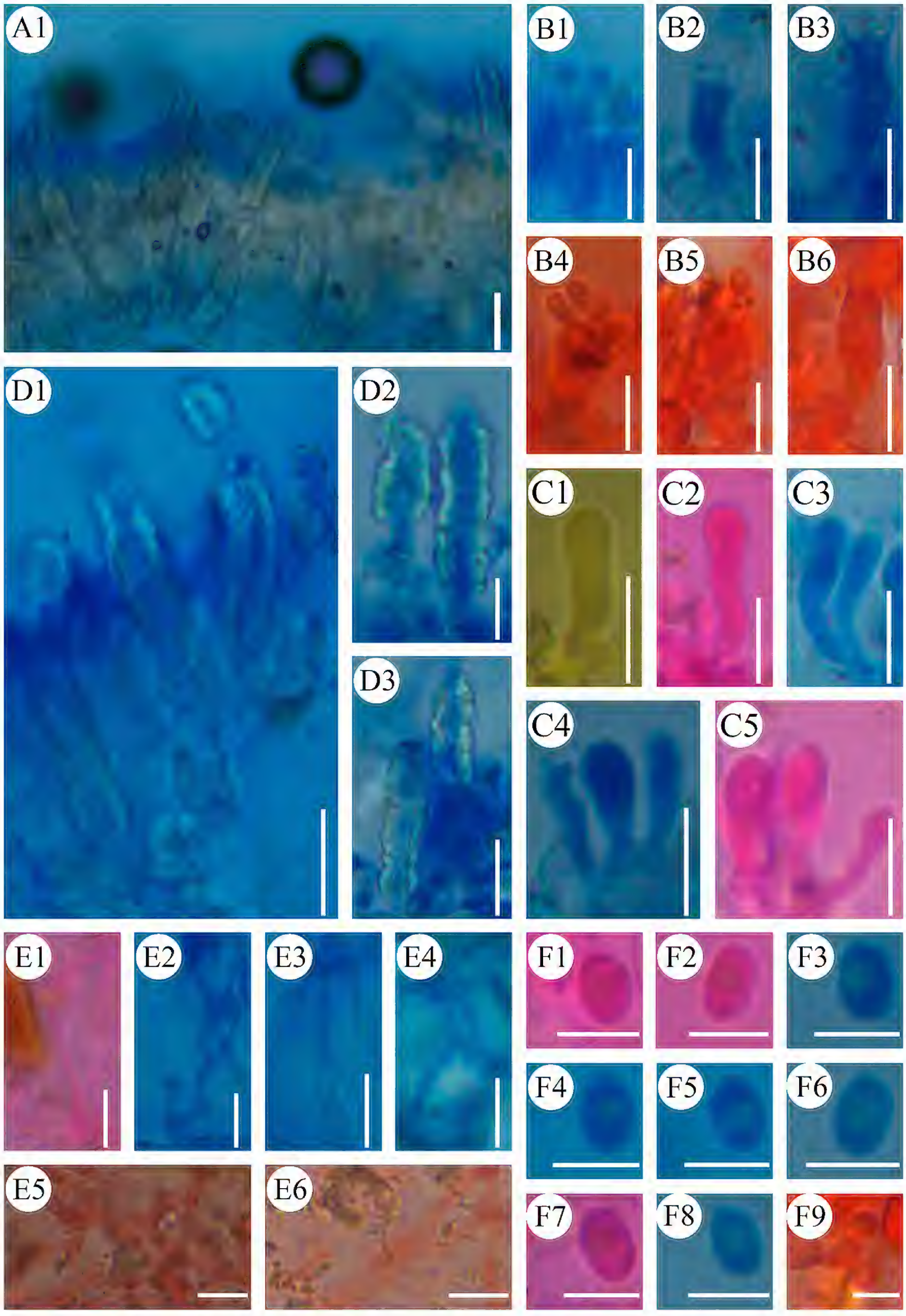

Figure 3. Microscopic structures of *Cystidichaete alba* (CLZhao 39667, holotype). **A1.** A section of the hymenium; **B1–B6.** Basidia; **C1–C5.** Basidioles; **D1–D3.** Lamprocystidia; **E1–E4.** Subicular hyphae; **E5, E6.** Hyphae; **F1–F9.** Basidiospores. Scale bars: 20 μm (**A1**); 10 μm (**B1–B6**) 10 μm (**C1–C5**); 20 μm (**D1, D3**); 10 μm (**D2**); 10 μm (**E1–E6**); 5μm (**F1–F9**).

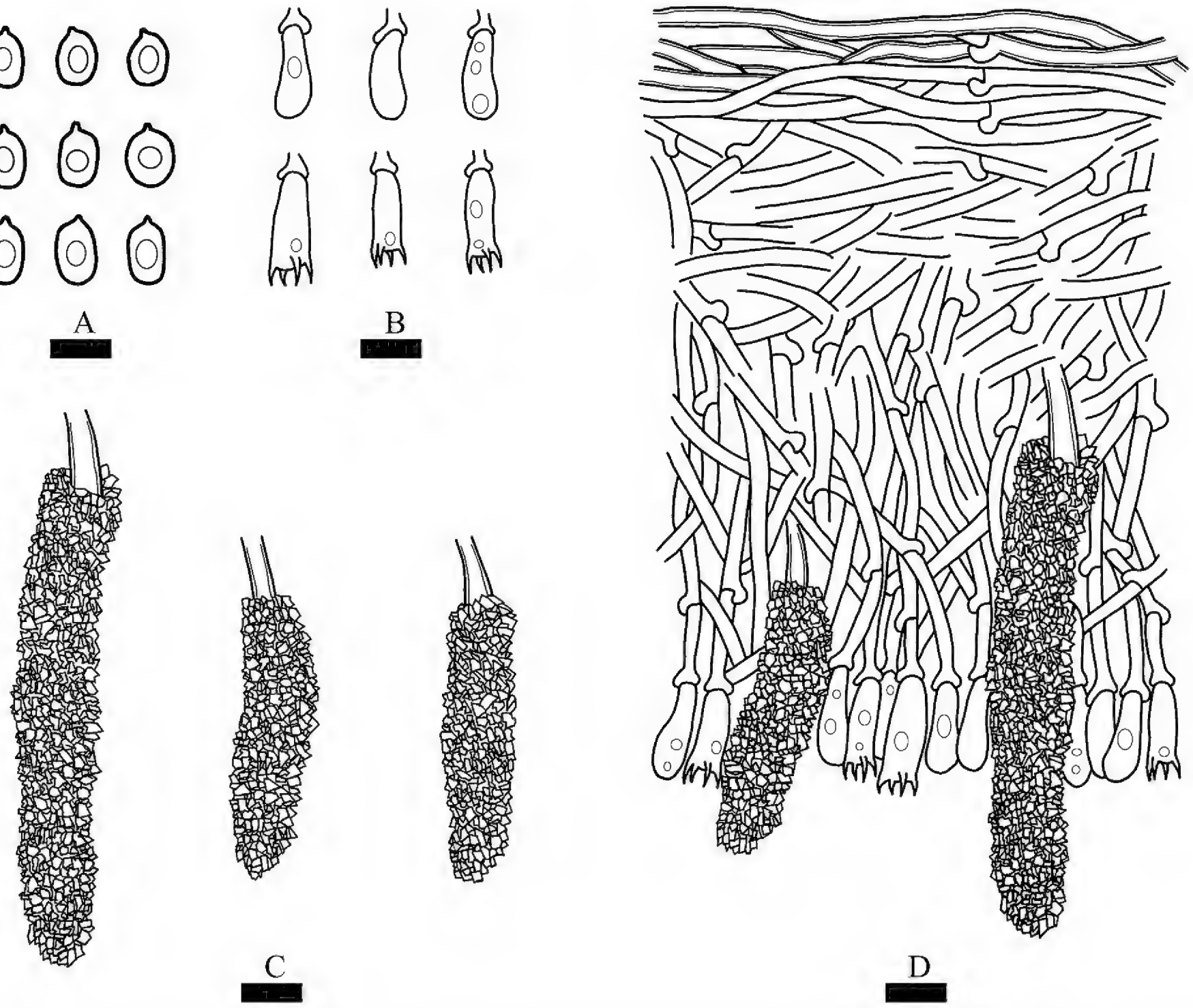

Figure 4. Microscopic structures of *Cystidichaete alba* (Drawn from the holotype CLZhao 39667). **A.** Basidiospores; **B.** Basidia and basidioles; **C.** Lamprocystidia; **D.** Section through basidioma. Scale bars: 5 µm (**A**); 10 µm (**B–D**).

Basidiospores. Ellipsoid, colorless, smooth, thin-walled, often with oily drops, IKI−, CB−, (4−)4.4−5.8(−6) × (2−)2.5−3.8(−4) µm, L = 5.10 µm, W = 3.20 µm, Q = 1.59, Qm = 1.59 ± 0.05 (n = 30/1).

Type of rot. White rot.

Additional specimen (paratype) examined. CHINA • Yunnan Province, Dehong Dai and Jingpo Autonomous Prefecture, Mangshi, Tongbiguan Nature Reserve, GPS coordinates 24°22'N, 97°50'E, altitude 1405 m asl., on fallen angiosperm branch, leg. C.L. Zhao, 8 July 2024, CLZhao 39422 (SWFC 00039422).

Discussion

The Dehong Dai and Jingpo Autonomous Prefecture, located in Southwestern China, is renowned as one of the most biologically diverse regions in the country. Its topography and diverse ecosystems, making it a focal point for fungal biodiversity in China. Recently, studies on fungal diversity and the ecology of Basidiomycota in Dehong, Yunnan Province, were conducted (Chen et al. 2025; Deng et al. 2025; Gu et al. 2025; Liu et al. 2025a, 2025b; Xu et al. 2025; Yang et al. 2025b). Integrated scientific research indicated that Tongbiguan Nature Reserve features tall trees and vertically zoned vegetation succession, encom-

passing tropical monsoon forests, tropical montane rainforests, south-subtropical monsoon evergreen broad-leaved forests, mid-mountain humid evergreen broad-leaved forests, bamboo forests, shrublands, and grasslands, in which this heterogeneous habitat fosters exceptional macrofungal diversity (Yang and Du 2006).

The generic-level phylogeny of Phanerochaetaceae has become increasingly well resolved, with several new genera erected to accommodate independent lineages (Floudas and Hibbett 2015; Miettinen et al. 2016; Yuan et al. 2017; Chen et al. 2018, 2021; Ma and Zhao 2019; Dong et al. 2024, 2025b; Luo et al. 2024; Xu et al. 2025). At present, 29 genera are accepted in the family, most of which are corticioid fungi (Chen et al. 2021; Xu et al. 2025). Although most of the newly described taxa in the family originated from East Asia, several lineages in this region still require further systematic study based on more comprehensive sampling. Our multilocus phylogenetic analyses using combined ITS+nLSU+*rpb2*+*tef1-α* sequences analysis (Fig. 1), placed the new genus and its novel species within Phanerochaetaceae (Polyporales, Basidiomycota).

Phylogenetically, the phylogram based on the combined ITS+nLSU+*rpb2*+*tef1-α* dataset showed that *Cystidichaete alba* clustered with *Stereophlebia pendula* (Fr.) K.H. Larss and *Gelatinofungus brunneus* Sheng H. Wu, C.C. Chen & C.L. Wei with strong support (100% BS, 97% BP, 1.00 BPP; Fig.1). However, *Stereophlebia pendula* differs from *Cystidichaete alba* by its effused to effused reflexed, membranous basidiomata, hymenium smooth to tuberculate, sometimes with radiating ridges near the margin, cream to ochraceous to pale orange reddish, pileus surface smooth with adpressed hyphae and longer basidiospores (5.7–7.1 × 2.7–3.3 µm vs. 4.4–5.8 × 2.5–3.8 µm; Larsson et al. 2025). *Gelatinofungus brunneus* differs from *Cystidichaete alba* by its ceraceous basidiomata, hymenial surface dark purplish gray with brownish tints when young, becoming cinnamon to brown when old, darkening in KOH, tuberculate, uncracked and longer basidia (20–38 × 5–6 µm vs. 13–20× 4–6 µm) (Chen et al. 2021).

Phanerochaetaceae is a major group of wood-inhabiting fungi (Basidiomycota) characterized by relatively simple basidiomata and fewer diagnostic morphological features than those of polypores and mushrooms (Xu et al. 2020). Despite this morphological simplicity, they exhibit higher species and phylogenetic diversity, yet remain substantially understudied (Larsson et al. 2004; Binder et al. 2005; Bernicchia and Gorjón 2010; Dai 2011; Sun et al. 2020). A substantial number of Phanerochaetaceae remain undocumented worldwide, particularly in subtropical and tropical ecosystems (Dong et al. 2024; Zhou et al. 2024; Yang et al. 2025b). As shown in this study and earlier ones (Volobuev et al. 2015; Chen et al. 2018; Xu et al. 2025), DNA sequence data are invaluable for resolving cryptic diversity and delimiting taxa within Phanerochaetaceae. Therefore, future taxonomic studies should continue to integrate detailed morphological assessments with multilocus phylogenetic analyses to better document species diversity and to refine our understanding of the phylogeny and evolutionary history of the family.

Additional information

Conflict of interest

The authors have declared that no competing interests exist.

Ethical statement

No ethical statement was reported.

Use of AI

No use of AI was reported.

Funding

The research was supported by the Modern Industry School of Edible-fungi, Southwest Forestry University (Project No. SYJ25), Forestry and Grass Science and Technology Innovation Joint Project of Yunnan Province (Project No. 202404CB090008) and Yunnan Province College Students Innovation and Entrepreneurship Training Program (Project No. s202310677028).

Author contributions

Conceptualization, C.Z.; methodology, C.Z. and X.Z.; software, C.Z., and X.Z.; validation, C.Z. and X.Z.; formal analysis, C.Z., X.Z. and D.C.; investigation, C.Z., X.Z. and D.C.; resources C.Z.; writing – original draft preparation, C.Z. and X.Z.; writing – review and editing, C.Z. and X.Z.; visualization, C.Z.; supervision, C.Z.; project administration, C.Z.; funding acquisition, C.Z. All authors have read and agreed to the published version of the manuscript.

Author ORCIDs

Xunchi Zhang https://orcid.org/0000-0003-3887-0979
Daxiang Chen https://orcid.org/0009-0001-2309-1991
Changlin Zhao https://orcid.org/0000-0002-8668-1075

Data availability

All of the data that support the findings of this study are available in the main text.

References

An Q, Wu XJ, Wu B, Dai YC (2015) Effects of carbon and nitrogen sources on lignocellulose decomposition enzyme activities in *Flammulina velutipes*. Mycosystema 34(4): 761–771.

Bernicchia A, Gorjón SP (2010) Fungi Europaei 12: Corticiaceae s.l. Edizioni Candusso, Alassio, 1–1008.

Binder M, Hibbet DS, Larsson KH, Larsson E, Langer E, Langer G (2005) The phylogenetic distribution of resupinate forms across the major clades of mushroom-forming fungi (Homobasidiomycetes). Systematics and Biodiversity 3: 113–157. https://doi.org/10.1017/S1477200005001623

Binder M, Justo A, Riley R, Salamov A, Lopez-Giraldez F, Sjökvist E, Copeland A, Foster B, Sun H, Larsson E, Larsson KH, Townsend J, Grigoriev IV, Hibbett DS (2013) Phylogenetic and phylogenomic overview of the Polyporales. Mycologia 105: 1350–1373. https://doi.org/10.3852/13-003

Brandon Matheny P, Wang Z, Binder M, Curtis JM, Lim YW, Henrik Nilsson R, Hughes KW, Hofstetter V, Ammirati JF, Schoch CL, Langer E, Langer G, McLaughlin DJ, Wilson AW, Frøslev T, Ge ZW, Kerrigan RW, Slot JC, Yang ZL, Baroni TJ, Fischer M, Hosaka K, Matsuura K, Seidl MT, Vauras J, Hibbett DS (2007) Contributions of *rpb2* and *tef1* to

the phylogeny of mushrooms and allies (Basidiomycota, Fungi). Molecular Phylogenetics and Evolution 43: 430–451. https://doi.org/10.1016/j.ympev.2006.08.024

Bucher VVC, Hyde KD, Pointing SB, Reddy CA (2004) Production of wood decay enzymes, mass loss and lignin solubilization in wood by marine ascomycetes and their anamorphs. Microbial Ecology 48(3): 331–337. https://doi.org/10.1007/s00248-003-0132-x

Chen CC, Chen CY, Wu SH (2021) Species diversity, taxonomy and multi-gene phylogeny of phlebioid clade (Phanerochaetaceae, Irpicaceae, Meruliaceae) of Polyporales. Fungal Diversity 111: 337–442. https://doi.org/10.1007/s13225-021-00490-w

Chen CC, Wu SH, Chen CY (2018) *Hydnophanerochaete* and *Odontoefibula*, two new genera of phanerochaetoid fungi (Polyporales, Basidiomycota) from East Asia. MycoKeys 39: 75–96. https://doi.org/10.3897/MycoKeys.39.28010

Chen DX, Zhang SH, Yang RF, Li CJ, Yan ML, Dong JH, Zhao CL (2025) Molecular phylogeny and morphology reveal a new species of *Radulomyces* (Radulomycetaceae, Agaricales) from Southwestern China. Phytotaxa 696(3): 205–216. https://doi.org/10.11646/phytotaxa.696.3.1

Chen R, He X, Zhao CL (2022) *Callosus wenshanensis* gen. & sp. nov. from China. Mycotaxon 137: 435–448. https://doi.org/10.5248/137.435

Cui BK, Li HJ, Ji X, Zhou JL, Song J, Si J, Yang ZL, Dai YC (2019) Species diversity, taxonomy and phylogeny of Polyporaceae (Basidiomycota) in China. Fungal Diversity 97: 137–392. https://doi.org/10.1007/s13225-019-00427-4

Dai YC (2010) Hymenochaetaceae (Basidiomycota) in China. Fungal Diversity 45: 131–343. https://doi.org/10.1007/s13225-010-0066-9

Dai YC (2011) A revised checklist of corticioid and hydnoid fungi in China for 2010. Mycoscience 52: 69–79. https://doi.org/10.1007/s10267-010-0068-1

Dai YC, Yang ZL, Cui BK, Wu G, Yuan HS, Zhou LW, He SH, Ge ZW, Wu F, Wei YL, Yuan Y, Si J (2021) Diversity and systematics of the important macrofungi in Chinese forests. Mycosystema 40: 770–805. https://doi.org/10.13346/j.mycosystema.210036

Deep White Printing Team (2022) Completee prooceess color chart & Four-color superimposition gold and silver. High Color International Publishing House, Hong Kong. 135 pp.

Deng YL, Chen M, Liu LF, Li QZ, Zhang SC, Yuan HS, Zhao CL (2025) Morphological and molecular analyses revealed four new wood-inhabiting fungal species (Hymenochaetales, Basidiomycota) from Yunnan. MycoKeys 117: 29–66. https://doi.org/10.3897/mycokeys.117.146236

Dong JH, Li Q, Yuan Q, Luo YX, Zhang XC, Dai YF, Zhou Q, Liu XF, Deng YL, Zhou HM, Muhammad A, Zhao CL (2024) Species diversity, taxonomy, molecular systematics and divergence time of wood-inhabiting fungi in Yunnan-Guizhou Plateau, Asia. Mycosphere 15(1): 1110–1293. https://doi.org/10.5943/mycosphere/15/1/10

Dong JH, Xu Y, Jiang QQ, Hosen MI, Zhao CL (2025a) A new genus and two new species of Auriculariales (Basidiomycota) from southwest China, evidenced by morphological characteristics and phylogenetic analyses. Mycological Progress 24: 4. https://doi.org/10.1007/s11557-024-02027-2

Dong JH, Chen ML, Chen M, Li Q, Zhu YJ, Zhang XC, Zhou CQ, Li W, Muhammad A, Zhou HM, Jabeen S, Zhao CL (2025b) Notes, outline, taxonomy and phylogeny of wood inhabiting Agaricales. Mycosphere 16(1): 2599–2711. https://doi.org/10.5943/mycosphere/16/1/16

Felsenstein J (1985) Confidence intervals on phylogenetics: An approach using boot strap. Evolution 39(4): 783–791. https://doi.org/10.2307/2408678

Floudas D, Hibbett DS (2015) Revisiting the taxonomy of *Phanerochaete* (Polyporale Basidiomycota) using a four gene dataset and extensive ITS sampling. Fungal Biology 119: 679–719. https://doi.org/10.1016/j.funbio.2015.04.003

Gu ZR, Zhou CQ, Zhang JL, Liu Y, Deng QH, Yang RC, Yang SQ, Zhao CL (2025) Taxonomy and phylogeny of Irpicaceae and Meruliaceae (Polyporales, Basidiomycota) with descriptions of four new species from southwestern China. MycoKeys 119: 197–234. https://doi.org/10.3897/mycokeys.119.157018

He MQ, Cao B, Liu F, Boekhout T, Denchev TT, Schoutteten N, Denchev CM, Kemler M, Gorjón SP, Begerow D, Valenzuela R, Davoodian N, Niskanen T, Vizzini A, Redhead SA, Ramírez-Cruz V, Papp V, Dudka VA, Dutta AK, García-Sandoval R, Liu XZ, Kijpornyong pan T, Savchenko A, Tedersoo L, Theelen B, Trierveiler-Pereira L, Wu F, Zamora JC, Zeng XY, Zhou LW, Liu SL, Ghobad-Nejhad M, Giachini AJ, Li GJ, Kakishima M, Olariaga I, Haelewaters D, Sulistyo B, Sugiyama J, Svantesson S, Yurkov A, Alvarado P, Antonín V, da Silva AF, Druzhinina I, Gibertoni TB, Guzmán-Dávalos L, Justo A, Karunarathna SC, Galappaththi MCA, Toome-Heller M, Hosoya T, Liimatainen K, Márquez R, Mešić A, Moncalvo JM, Nagy LG, Varga T, Orihara T, Raymundo T, Salcedo I, Silva-Filho AGS, Tkalčec Z, Wartchow F, Zhao CL, Bau T, Cabarroi-Hernández M, Cortés-Pérez A, De cock C, De Lange R, Weiss M, Menolli Jr N, Nilsson RH, Fan YG, Verbeken A, Gafforov Y, Meiras-Ottoni A, Mendes-Alvarenga RL, Zeng NK, Wu Q, Hyde KD, Kirk PM, Zhao RL (2024) Phylogenomics, divergence times and notes of orders in Basidiomycota. Fungal Diversity 126: 127–406. https://doi.org/10.1007/s13225-024-00535-w

Horak E (2005) Röhrlinge und Blätterpilze in Europa: Bestimmungsschlüssel für Polyporales (p.p.), Boletales, Agaricales, Russulales. Elsevier, Spektrum, Akad. Verlag, 575 pp.

Hyde KD (2022) The numbers of fungi. Fungal Diversity 114: 1. https://doi.org/10.1007/s13225-022-00507-y

Hyde KD, Noorabadi MT, Thiyagaraja V, He MQ, Johnston PR, Wijes inghe SN, Armand A, Biketova AY, Chethana KWT, Erdoğdu M, Ge ZW, Groenewald JZ, Hongsanan S, Kušan I, Leontyev DV, Li DW, Lin CG, Liu NG, Maharachchikumbura SSN, Matočec N, MayTW, McKenzie EHC, Mešić A, Perera RH, Phukhamsakda C, Piątek M, Samarakoon MC, Selcuk F, Senanayake IC, Tan ney JB, Tian Q, Vizzini A, Wanasinghe DN, Wannasawang N, Wijayawardene NN, Zhao RL, Abdel-Wahab MA, Abdollahzadeh J, Abeywickrama PD, Abhinav, Absalan S, Acharya K, Afshari N, Afshan NS, Afzalinia S, Ahmadpour SA, Akulov O, Alizadeh A, Alizadeh M, Al-Sadi AM, Alves A, Alves VCS, Alves-Silva G, Antonín V, Aouali S, Aptroot A, Apurillo CCS, Arias RM, Asgari B, Asghari R, Assis DMA, Assyov B, Atienza V, Aumentado HDR, Avasthi S, Azevedo E, Bakhshi M, Bao DF, Baral HO, Barata M, Barbosa KD, Barbosa RN, Barbosa FR, Baroncelli R, Barreto GG, Baschien C, Bennett RM, Bera I, Bezerra JDP, Bhun jun CS, Bianchinotti MV, Błaszkowski J, Boekhout T, Bonito GM, Boonmee S, Boonyuen N, Bortnikov FM, Bregant C, Bundhun D, Burgaud G, Buyck B, Caeiro MF, Cabarroi-Hernández M, Cai MF, Cai L, Calabon MS, Calaça FJS, Callalli M, Câmara MPS, Cano-Lira J, Cao B, Carlavilla JR, Carvalho A, Carvalho TG, Castañeda-Ruiz RF, Catania MDV, Cazabonne J, Cedeño Sanchez M, Chaharmiri-Dokhaharani S, Chaiwan N, Chakraborty N, Cheewankoon R, Chen C, Chen J, Chen Q, Chen YP, China glia S, Coelho-Nascimento CC, Coleine C, CostaRezende DH, Cortés-Pérez A, Crouch JA, Crous PW, Cruz RHSF, Czachura P, Damm U,Darmostuk V, Daroodi Z, Das K, Das K, Davoodian N, Davydov EA, da Silva GA, da Silva IR, daSilva RMF, da Silva Santos AC, Dai DQ, Dai YC, de Groot Michiel D, De Kesel A, De Lange R, de Medeiros EV, de Souza CFA, de Souza FA, de Cruz TEE, Decock C, Delgado G, Denchev CM, Denchev TT, Deng YL, Dentinger BTM, Devadatha B, Dianese JC, Dima B, Iom M, Dissanayake AJ, Dissanayake DMLS, Dissanayake LS,

Diniz AG, Dolatabadi S, Dong JH, Dong W, Dong ZY, Drechsler Santos ER, Druzhinina IS, Du TY, Dubey MK, Dutta AK, Elliott TF, Elshahed MS, Egidi E, Eisvand P, Fan L, Fan X, Fan XL, Fedosova AG, Ferro LO, Fiuza PO, Flakus AW, Fonseca EO, Fryar SC, Gabaldón T, Gajanayake AJ, Gannibal PB, Gao F, GarcíaSánchez D, García-Sandoval R, Garrido-Benavent I, Gar zoli L, Gasca-Pineda J, Gautam AK, GenéJ, Ghobad-Nejhad M, Ghosh A, Giachini AJ, Gibertoni TB, Gentekaki E, Gmoshinskiy VI, GóesNeto A, Gomdola D, Gorjón SP, Goto BT, Granados Montero MM, Griffith GW, Groenewald M, Grossart H-P, Gu ZR, Gueidan C, Gunarathne A, Gunaseelan S, Guo SL, Gusmão LFP, Gutierrez AC, Guzmán-Dávalos L, Haelewaters D, Haituk H, Halling RE, He SC, Heredia G, Hernández Restrepo M, Hosoya T, Hoog SD, Horak E, Hou CL, Houbraken J, Htet ZH, Huang SK, Huang WJ, Hurdeal VG, Hustad VP, Inácio CA, Janik P, Jayalal RGU, Jayasiri SC, Jayawardena RS, Jeewon R, Jerônimo GH, Jin J, Jones EBG, Joshi Y, Jurjević Ž, Justo A, Kakishima M, Kaliyaperumal M, Kang GP, Kang JC, Karimi O, Karunar athna SC, Karpov SA, Kezo K, Khalid AN, Khan MK, Khuna S, Khyaju S, Kirchmair M, Klawonn I, Kraisitudomsook N, Kukwa M, Kularathnage ND, Kumar S, Lachance MA, Lado C, Latha KPD, Lee HB, Leonardi M, Lestari AS, Li C, Li H, Li J, Li Q, Li Y, Li YC, Li YX, Liao CF, Lima JLR, Lima JMS, Lima NB, Lin L, Linaldeddu BT, Linn MM, Liu F, Liu JK, Liu JW, Liu S, Liu SL, Liu XF, Liu XY, Longcore JE, Luangharn T, Luangsa-ard JJ, Lu L, Lu YZ, Lumbsch HT, Luo L, Luo M, Luo ZL, Ma J, Mad agammana AD, Madhushan A, Madrid H, Magurno F, Magyar D, Mahadevakumar S, Malosso E, Malysh JM, Mamarabadi M, Manawasinghe IS, Manfrino RG, Manimohan P, Mao N, Mapook A, Marchese P, Marasinghe DS, Mardones M, Marin-Felix Y, Masigol H, Mehrabi M, MehrabiKoushki M, Meiras-Ottoni A, de Melo RFR, Mendes-Alvarenga RL, Mendieta S, Meng QF, Menkis A, Menolli Jr N, Mikšík M, Miller SL, Moncada B, Moncalvo JM, Monteiro JS, Monteiro M, Mora-Montes HM, Moroz EL, Moura JC, Muhammad U, Mukhopadhyay S, Nagy GL, Najamul Sehar A, Najafiniya M, Nanayakkara CM, Naseer A, Nascimento ECR, Nascimento SS, Neuhauser S, Neves MA, Niazi AR, Nie Y, Nilsson RH, Nogueira PTS, Novozhilov YK, Noordeloos M, Norphanphoun C, Nuñez Otaño N, O'Donnell RP, Oehl F, Oliveira JA, OliveiraJunior I, Oliveira NVL, Oliveira PHF, Orihara T, Oset M, Pang KL, Papp V, Pathirana LS, PeintnerU, Pem D, Pereira OL, Pérez-Moreno J, Pérez-Ortega S, Péter G, Pires-Zottarelli CLA, PhonemanyM, Phongeun S, Pošta A, Praz eres JFSA, Quan Y, Quandt CA, Queiroz MB, Radek R, Rahnama K, Raj KNA, Rajeshkumar KC, Rajwar S, Ralaiveloarisoa AB, Rämä T, Ramírez-Cruz V, Rambold G, Rathnayaka AR, Raza M, Ren GC, Rinaldi AC, Rivas-Ferreiro M, Robledo GL, Ronikier A, Rossi W, Rusevska K, Ryberg M, Safi A, Salimi F, Salvador Montoya CA, Samant B, Samaradiwakara NP, Sánchez-Castro I, Sandoval-Denis M, Santiago ALCMA, Santos ACDS, Santos LA dos, Sarma VV, Sarwar S, Savchenko A, Savchenko K, Saxena RK, Schoutteten N, Selbmann L, Ševčíková H, Sharma A, Shen HW, Shen YM, Shu YX, Silva HF, Silva-Filho AGS, Silva VSH, Simmons DR, Singh R, Sir EB, Sohrabi M, Souza FA, Souza Motta CM, Sriindrasutdhi V, Sruthi OP, Stadler M, Stemler J, Stephenson SL, Stoyneva-Gaertner MP, Strassert JFH, Stryjak Bogacka M, Su H, Sun YR, Svantesson S, Sysouphanthong P, Takamatsu S, Tan TH, Tanaka K, Tang C, Tang X, Taylor JE, Taylor PWJ, Tennakoon DS, Thakshila SAD, Thambugala KM, Thamodini GK, Thilanga D, Thines M, Tiago PV, Tian XG, Tian WH, Tibpromma S, Tkalčec Z, Tokarev YS, Tomšovský M, Tor ruella G, Tsurykau A, Udayanga D, Ulukapı M, Untereiner WA, Usman M, Uzunov BA, Vadthanarat S, Valenzuela R, Van den Wyngaert S, Van Vooren N, Velez P, Verma RK, Vieira LC, Vieira WAS, Vinzelj JM, Tang AMC, Walker A, Walker AK, Wang QM, Wang Y, Wang XY, Wang ZY, Wannathes N, Wartchow F, Weera koon G, Wei DP, Wei X, White JF, Wijesundara DSA, Wisitras sameewong K, Worobiec G, Wu HX, Wu N, Xiong YR, Xu B,

Xu JP, Xu R, Xu RF, Xu RJ, Yadav S, Yakovchenko LS, Yang HD, Yang X, Yang YH, Yang Y, Yang YY, Yoshioka R, Youssef Noha H, Yu FM, Yu ZF, Yuan LL, Yuan Q, Zabin DA, Zamora JC, Zapata CV, Zare R, Zeng M, Zeng XY, Zhang JF, Zhang JY, Zhang S, Zhang XC, Zhao CL, Zhao H, Zhao Q, Zhao H, Zhao HJ, Zhou HM, Zhu XY, Zmitrovich IV, Zucconi L, Zvyagina E (2024) The 2024 outline of fungi and fungus-like taxa. Mycosphere 15(1): 5146–6239. https://doi.org/10.5943/mycosphere/15/1/25

James TY, Stajich JE, Hittinger CT, Rokas A (2020) Toward a fully resolved fungal tree of life. Annual Review of Microbiology 74(1): 291–313. https://doi.org/10.1146/annurev-micro-022020-051835

Jia BS, Zhou LW, Cui BK, Rivoire B, Dai YC (2014) Taxonomy and phylogeny of Ceripori (Polyporales, Basidiomycota) with an emphasis of Chinese collections. Mycological Progres 13: 81–93. https://doi.org/10.1007/s11557-013-0895-5

Jülich W (1982) Higher taxa of Basidiomycetes. Bibliotheca Mycologica 85: 1–485.

Justo A, Miettinen O, Floudas D, Ortiz-Santana B, Sjökvist E, Lindner D, Nakasone KK, Niemelä T, Larsson KH, Ryvarden L, Hibbett DS (2017) A revised family-level classifcation of the Polyporales (Basidiomycota). Fungal Biology 121: 798–824. https://doi.org/10.1016/j.funbio.2017.05.010

Kalyaanamoorthy S, Minh BQ, Wong TKF, von Haeseler A, Jermiin LS (2017) ModelFinder: fast model selection for accurate phylogenetic estimates. Nature Methods 14: 587–589. https://doi.org/10.1038/nmeth.4285

Katoh K, Rozewicki J, Yamada KD (2019) MAFFT online service: Multiple sequence alignment, interactive sequence choice and visualization. Briefings in Bioinformatics 20(4): 1160–1166. https://doi.org/10.1093/bib/bbx108

Larsson A (2014) AliView: A fast and lightweight alignment viewer and editor for large data sets. Bioinformatics (Oxford, England) 30: 3276–3278. https://doi.org/10.1093/bioinformatics/btu531

Larsson KH (2007) Re-thinking the classifcation of corticioid fungi. Mycological Research 111: 1040–1063. https://doi.org/10.1016/j.mycres.2007.08.001

Larsson KH, Larsson E, Koljalg U (2004) High phylogenetic diversity among corticioid homobasidiomycetes. Mycological Research 108: 983–1002. https://doi.org/10.1017/S0953756204000851

Larsson KH, Spirin V, Ryvarden L, Larsson E (2025) Reclassification of eleven corticioid basidiomycetes with nine typifications. Fungal Systematics and Evolution 16: 1–27. https://doi.org/10.3114/fuse.2025.16.1

Li T, Jia LG, Jie HH, Lei G, Zou J, Wu XJ (2021) *Phlebiopsis Xuefengensis* sp. nov. from *Gastrodia elata* (Orchidaceae) in Hunan Province, Southern China. South African Journal of Botany 142: 299–304. https://doi.org/10.1016/j.sajb.2021.06.034

Liu S, Chen YY, Sun YF, He XL, Song CG, Si J, Liu MD, Gates G, Cui BK (2023) Systematic classification and phylogenetic relationships of the brown-rot fungi within the Polyporales. Fungal Diversity 118: 1–94. https://doi.org/10.1007/s13225-022-00511-2

Liu S, Cui BK, Zhu B (2025) Morphological characters and molecular data reveal ten new forest macrofungi species from Hebei Province, North China. Mycology 16(2): 690–737. https://doi.org/10.1080/21501203.2024.2390967

Liu YJ, Whelen S, Hall BD (1999) Phylogenetic relationships among ascomycetes: Evidence from an RNA polymerase II subunit. Molecular Biology and Evolution 16: 1799–1808. https://doi.org/10.1093/oxfordjournals.molbev.a026092

Liu ZB, Yuan Y, Dai YC, Liu HG, Vlasák J, Zeng GY, He SH, Wu F (2025a) Global diversity and systematics of Hymenochaetaceae with non-poroid hymenophore. Fungal Diversity. https//doi.org/10.1007/s13225-025-00552-3

Liu ZB, Liu HG, Vlasák J, Gates GM, Dai YC, Yuan Y (2025b) Global diversity and phylogeny of Incrustoporiaceae (Polyporales, Basidiomycota) with an emphasis on Skeletocutis. Mycology 16(3): 1083–1140. https://doi.org/10.1080/21501203.2024.2448145

Luo KY, Zhang X, Dai YC, Yuan Y (2024) Four new species of *Phanerochaete* (Polyporales, Basidiomycota) from China. MycoKeys 111: 41–64. https://doi.org/10.3897/mycokeys.111.133093

M'Barek HN, Arif S, Taidi B, Hajjaj H (2020) Consolidated bioethanol production from olive mill waste: wood-decay fungi from central Morocco as promising decomposition and fermentation biocatalysts. Biotechnology Reports 28: e00541. https://doi.org/10.1016/j.btre.2020.e00541

Ma X, Zhao CL (2019) *Crepatura ellipsospora* gen. et sp. nov. in Phanerochaetaceae (Polyporales, Basidiomycota) bearing a tuberculate hymenial surface. Mycological Progress 18: 785–793. https://doi.org/10.1007/s11557-019-01488-0

Miettinen O, Spirin V, Vlasák J, Rivoire B, Stenroos S, Hibbett D (2016) Polypores and genus concepts in Phanerochaetaceae (Polyporales, Basidiomycota). MycoKeys 17: 1–46. https://doi.org/10.3897/MycoKeys.17.10153

Miller MA, Pfeiffer W, Schwartz T (2012) The CIPRES science gateway: Enabling high impact science for phylogenetics researchers with limited resources. Association for Computing Machinery 39: 1–8. https://doi.org/10.1145/2335755.2335836

Niego AGT, Lambert C, Mortimer P, Thongklang N, Rapior S, Grosse M, Schrey H, Charria-Girón E, Walker A, Hyde KD, Stadler M (2023) The contribution of fungi to the global economy. Fungal Diversity 121: 95–137. https://doi.org/10.1007/s13225-023-00520-9

Parmasto E, Hallenberg N (2000) A taxonomic study of phlebioid fungi (Basidiomycota). Nordic Journal of Botany 20(1): 105–118. https://doi.org/10.1111/j.1756-1051.2000.tb00740.x

Petersen JH (1996) Farvekort. The Danish Mycological Society's Colour-Chart. Forenin gen til Svampekundskabens Fremme, Greve, Germany, 6 pp.

Rathnayaka AR, Tennakoon DS, Jones GE, Wanasinghe DN, Bhat DJ, Priyashantha AH, Stephenson SL, Tibpromma S, Karunarathna SC (2025) Significance of precise documentation of hosts and geospatial data of fungal collections, with an emphasis on plant-associated fungi. New Zealand Journal of Botany 63(2–3): 462–489. https://doi.org/10.1080/0028825X.2024.2381734

Rehner SA, Buckley E (2005) A Beauveria phylogeny inferred from nuclear ITS and EF1-alpha sequences: evidence for cryptic diversification and links to *Cordyceps* teleomorphs. Mycologia 97: 84–98. https://doi.org/10.3852/mycologia.97.1.84

Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, Höhna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP (2012) MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. Systematic Biology 61(3): 539–542. https://doi.org/10.1093/sysbio/sys029

Runnel K, Miettinen O, Lohmus A (2021) Polypore fungi as a flagship group to indicate changes in biodiversity – a test case from Estonia. IMA Fungus 12(2): 1–31. https://doi.org/10.1186/s43008-020-00050-y

Si J, Cui BK, He S, Dai YC (2011) Optimization of conditions for laccase production by *Perenniporia subacida* and its application in dye decolorization. Chinese Journal of Applied and Environmental Biology 17(5): 736–741. https://doi.org/10.3724/SP.J.1145.2011.00736

Sun YF, Costa-Rezende DH, Xing JH, Zhou JL, Zhang B, Gibertoni TB, Gates G, Glen M, Dai YC, Cui BK (2020) Multi-gene phylogeny and taxonomy of *Amauroderma* s.

lat. (Ganodermataceae). Persoonia 44: 206–239. https://doi.org/10.3767/persoonia.2020.44.08

Swofford DL (2002) PAUP*: Phylogenetic analysis using parsimony (*and Other Methods), Version 4.0b10, Sinauer Associates: Sunderland, MA, USA.

Telleria MT, Dueñas M, Melo I, Martín MP (2010) Morphological and molecular studies of *Hyphodermella* in the Western Mediterranean area. Mycological Progress 9: 585–596. https://doi.org/10.1007/s11557-010-0666-5

Větrovský T, Kolařík M, Žifčáková L, Zelenka T, Baldrian P (2016) The *rpb2* gene represents a viable alternative molecular marker for the analysis of environmental fungal communities. Molecular Ecology Resources 16(2): 388–401. https://doi.org/10.1111/1755-0998.12456

Vilgalys R, Hester M (1990) Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. Journal of Bacteriology 172(8): 4238–4246. https://doi.org/10.1128/jb.172.8.4238-4246.1990

Volobuev S, Okun M, Ordynets A, Spirin V (2015) The *Phanerochaete sordida* group (Polyporales, Basidiomycota) in temperate Eurasia, with a note on *Phanerochaete pallida*. Mycological Progress 14: 80. https://doi.org/10.1007/s11557-015-1097-0

White TJ, Bruns T, Lee S, Taylor J (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis MA, Gelfand DH, Sninsky JJ, White TJ (Eds) PCR protocols: A guide to methods and ap-plications. Academic Press, San Diego, 315–322. https://doi.org/10.1016/B978-0-12-372180-8.50042-1

Wijayawardene NN, Hyde KD, Al-Ani LKT, Tedersoo L, Haelewa ters D, Rajeshkumar KC, Zhao RL, Aptroot A, Leontyev DV, Saxena RK, Tokarev YS, Dai DQ, Letcher PM, Stephenson SL, Ertz D, Lumbsch HT, Kukwa M, Issi IV, Madrid H, Phillips AJL, Selbmann L, Pfliegler WP, Horváth E, Bensch K, Kirk PM, Kolaříková K, Raja HA, Radek R, Papp V, Dima B, Ma J, Malosso E, Takamatsu S, Rambold G, Gannibal PB, Triebel D, Gautam AK, Avasthi S, Suetrong S, Timdal E, Fryar SC, Delgado G, Réblová M, Doilom M, Dolatabadi S, Pawłowska J, Humber KR, Sánchez-Castro I, Goto BT, Silva DKA, de Souza FA, Oehl F, da Silva GA, Silva IR, Błaszkowski J, Jobim K, Maia LC, Bar bosa FR, Fiuza PO, Divakar PK, Shenoy BD, Castañeda-Ruiz RF, Somrithipol S, Lateef AA, Karunarathna SC, Tibpromma S, Mor timer PE, Wanasinghe DN, Phookamsak R, Xu J, Wang Y, Tian F, Alvarado P, Li DW, Kušan I, Matočec MSSN, Papizadeh M, Heredia G, Wartchow F, Bakhshi M, Boehm E, Youssef N, Hustad VP, Lawrey JD, Santiago ALCMA, Bezerra JDP, Souza-Motta CM, Firmino AL, Tian Q, Houbraken J, Hongsanan S, Tanaka K, Dissanayake AJ, Monteiro JS, Grossart HP, Suija A, Weerakoon G, Etayo J, Tsurykau A, Vázquez V, Mungai P, Damm U, Li QR, Zhang H, Boonmee S, Lu YZ, Becerra AG, Kendrick B, Brearley FQ, Motiejūnaitė J, Sharma B, Khare R, Gaikwad S, Wijesundara DSA, Tang LZ, He MQ, Flakus A, Rodriguez-Flakus P, Zhur benko MP, McKenzie EHC, Stadler M, Bhat DJ, Liu JK, Raza M, Jeewon R, Nassonova ES, Prieto M, Jayalal RGU, Erdoğdu M, Yurkov A, Schnittler M, Shchepin ON, Novozhilov YK, Silva Filho LP, Cavender JC, Kang Y, Mohammad S, Zhang LF, Xu RF, Li YM, Dayarathne MC, Ekanayaka AH, Wen TC, Deng CY, Pereira OL, Navathe S, Hawksworth DL, Fan XL, Dissan ayake LS, Kuhnert E, Grossart HP, Thines M (2020) Outline of fungi and fungus-like taxa. Mycosphere 11(1): 1060–1456. https://doi.org/10.5943/mycosphere/11/1/8

Wijayawardene NN, Hyde KD, Dai DQ, Sánchez-García M, Goto BT, Saxena RK, Erdoğdu M, Selçuk F, Rajeshkumar KC, Aptroot A, Błaszkowski J, Boonyuen N, da Silva GA, de Souza FA, Dong W4, Ertz D, Haelewaters D, Jones EBG, Karunarathna SC, Kirk PM, Kukwa M, Kumla J, Leontyev DV, Lumbsch HT, Maharach chikumbura SSN, Marguno F, Martínez-Rodríguez P, Mešić A, Monteiro JS, Oehl F, Pawłowska J, Pem D, Pfliegler

WP, Phil lips AJL, Pošta A, He MQ, Li JX, Raza M, Sruthi OP, Suetrong S, Suwannarach N, Tedersoo L, Thiyagaraja V, Tibpromma S, Tkalčec Z, Tokarev YS, Wanasinghe DN, Wijesundara DSA, Wimalaseana SDMK, Madrid H, Zhang GQ, Gao Y, Sánchez Castro I, Tang LZ, Stadler M, Yurkov A, Thines M (2022) Outline of fungi and fungus-like taxa – 2021. Mycosphere 13(1): 53–453. https://doi.org/10.5943/mycosphere/13/1/2

Wu F, Zhou LW, Yang ZL, Bau T, Li TH, Dai YC (2019) Resource diversity of Chinese macrofungi: edible, medicinal and poisonous species. Fungal Diversity 98: 1–76. https://doi.org/10.1007/s13225-019-00432-7

Xiang CY, Gao FL, Jakovlić I, Lei HP, Hu Y, Zhang H, Zou H, Wang GT, Zhang D (2023) Using PhyloSuite for molecular phylogeny and tree-based analyses. iMeta 2(1): e87. https://doi.org/10.1002/imt2.87

Xu YL, Cao YF, Nakasone KK, Chen CC, He SH (2020) Taxonomy and phylogeny of Phanerochaete sensu stricto with emphasis on Chinese collections and descriptions of nine new species. Mycosphere 11(1): 1527–1552. https://doi.org/10.5943/mycosphere/11/1/12

Xu Y, Yang Y, Yang X, Chen DX, Zheng W, Shen K, Zhang SC, Zhao CL (2025) Molecular phylogeny and taxonomy reveal two new genera and five new species in Phanerochaetaceae (Polyporales) from Yunnan, Southwest China. MycoKeys 113: 263–294. https://doi.org/10.3897/mycokeys.113.140624

Yang X, Duan SJ, Li M, Li DX, Yang RC, Zhang SH, Xu TM, Li W, Zhou HM, Zhao CL (2025a) A new genus and three new species of Lycoperdaceae (Agaricales) from Southern China revealed by molecular phylogeny and taxonomy. MycoKeys 118: 147–177. https://doi.org/10.3897/mycokeys.118.153703

Yang Y, Xu Y, Wang L, Jiang QQ, Su JQ, Li R, Zhou HM, Zhao CL (2025b) Multigene phylogeny of seven wood-inhabiting fungal orders in Basidiomycota, and proposal of a new genus and thirteen new species. Mycosphere 16(1): 245–295. https://doi.org/10.5943/mycosphere/16/1/4

Yang YM, Du F (2006) Integrated scientific studies indicates Tongbiguan Nature Reserve features. Yunnan Science and Technology Press, Yunnan, 467 pp.

Yuan Y, Chen JJ, He SH (2017) *Geliporus exilisporus* gen. et comb. nov., a xanthochroic polypore in Phanerochaetaceae from China. Mycoscience 58: 197–203. https://doi.org/10.1016/j.myc.2017.01.006

Yuan Y, Bian LS, Wu YD, Chen JJ, Wu F, Liu HG, Zeng GY, Dai YC (2023) Species diversity of pathogenic wood-rotting fungi (Agaricomycetes, Basidiomycota) in China. Mycology 14(3): 204–226. https://doi.org/10.1080/21501203.2023.2238779

Zhang D, Gao F, Jakovlić I, Zou H, Zhang J, Li WX, Wang GT (2020) PhyloSuite: An integrated and scalable desktop platform for streamlined molecular sequence data management and evolutionary phylogenetics studies. Molecular Ecology Resources 20(1): 348–355. https://doi.org/10.1111/1755-0998.13096

Zhao CL, Qu MH, Huang RX, Karunarathna SC (2023) Multi-gene phylogeny and taxonomy of the wood-rotting fungal genus *Phlebia* sensu lato (Polyporales, Basidiomycota). Journal of Fungi 9(3): 320. https://doi.org/10.3390/jof9030320

Zhao CL, Wu ZQ (2017) *Ceriporiopsis kunmingensis* sp. nov. (Polyporales, Basidiomyco ta) evidenced by morphological characters and phylogenetic analysis. Mycological Progress 16: 93–100. https://doi.org/10.1007/s11557-016-1259-8

Zhao H, Wu YD, Yang ZR, Liu HG, Wu F, Dai YC, Yuan Y (2024) Polypore funga and species diversity in tropical forest ecosystems of Africa, America and Asia, and a comparison with temperate and boreal regions of the Northern Hemisphere. Forest Ecosystems 11: 100200. https://doi.org/10.1016/j.fecs.2024.100200

Zhou HM, Zhang XC, Li JT, Wu F, Zhao CL (2024) Morphological characteristics and phylogenetic analyses revealed four new wood inhabiting fungi (Agaricomycetes, Basidiomycota) in Xizang Autonomous Region, China. MycoKeys 106: 201–224. https://doi.org/10.3897/mycokeys.106.125831

Zmitrovich IV (2018) Conspectus systematis Polyporacearum v. 1.0. Folia Cryptogamica Petropolitana 6: 3–145.